# *B O A D I C E A*

## RISK MODELLING SOFTWARE ON THE WORLD WIDE WEB

**BOADICEA Web Application version 3.0**
**January 2014**

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# BOADICEA PUBLICATIONS

This user guide describes BOADICEA Web Application version 3.0 (BWA 3.0).

BWA 3.0 is described in this paper:

**Users should cite this paper when describing results generated with BWA 3.0:**

Lee AJ, Cunningham AP, Kuchenbaecker KB, Mavaddat N, Easton DF, Antoniou AC, The Consortium of Investigators of Modifiers of BRCA1/21 and The Breast Cancer Association Consortium, BOADICEA breast cancer risk prediction model: updates to cancer incidences, tumour pathology and web interface, British Journal of Cancer, online publication 17 December 2013 (doi:10.1038/bjc.2013.730).

Available online here

BWA 3.0 uses technology described in this paper:

Mavaddat N, Rebbeck TR, Lakhani SR, Easton DF, Antoniou AC, Incorporating tumour pathology information into breast cancer risk prediction algorithms, Breast Cancer Research, online publication 18 May 2010 (doi: 10.1186/bcr2576).

Available online here

BWA 3.0 incorporates data described in this paper:

Mavaddat N, Barrowdale D, Andrulis IL, Domchek SM, Eccles D, Nevanlinna H, Ramus SJ, Spurdle A, Robson M, Sherman M *et al.* Consortium of Investigators of Modifiers of BRCA1/2, Pathology of breast and ovarian cancers among BRCA1 and BRCA2 mutation carriers: results from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA), Cancer Epidemiology, Biomarkers & Prevention, online publication 5 December 2011 (doi: 10.1158/1055-9965.EPI-11-0775 ).

Available online here

This paper describes the BWA software development process:

Cunningham AP, Antoniou AC and Easton, DF. 2012. Clinical software development for the Web: lessons learned from the BOADICEA project, *BMC Medical Informatics and Decision Making*, **12**:30, doi:10.1186/1472-6947-12-30.

Available online here

A validation study describing the performance of BOADICEA for breast cancer risk prediction is described in this paper:

MacInnis RJ, Bickerstaffe A, Apicella C, Dite GS, Dowty JG, Aujard K, Phillips K-A, Weideman P, Lee A, Terry MB, Giles GG, Southey MC, Antoniou AC and Hopper JL, Prospective validation of the breast cancer risk prediction model BOADICEA and a batch-mode version BOADICEACentre, British Journal of Cancer, published online 13 August 2013 (doi:10.1038/bjc.2013.382).

Available online here

A validation study describing the performance of BOADICEA and other risk models is described in this paper:

Antoniou A., Hardy R., Walker L., Evans D.G., Shenton A., Eeles R., Shanley S., Pichert G., Izatt L., Rose S., Douglas F., Eccles D., Morrison P., Scott J., Zimmern R., Easton D. and Pharoah P., Predicting the likelihood of carrying a BRCA1 or BRCA2 mutation: validation of BOADICEA, BRCAPRO, IBIS, Myriad and the Manchester scoring system using data from UK genetics clinics, Journal of Medical Genetics, advance online publication 15 April 2008 (doi:10.1136/jmg.2007.056556).

Available online via PubMed here

BWA 2.0 (previous version) is described in this paper:

Antoniou AC, Cunningham AP, Peto J, Evans DG, Lalloo F, Narod SA, Risch HA, Eyfjord JE, Hopper JL, Southey MC, Olsson H, Johannsson O, Borg A, Passini B, Radice P, Manoukian S, Eccles DM, Tang N, Olah E, Anton-Culver H, Warner E, Lubinski J, Gronwald J, Gorski B, Tryggvadottir L, Syrjakoski K, Kallioniemi O-P, Eerola H, Nevanlinna H, Pharoah PDP and Easton DF, The BOADICEA model of genetic susceptibility to breast and ovarian cancers: updates and extensions, British Journal of Cancer, advance online publication 18 March 2008 (doi: 10.1038/sj.bjc.6604305).

Available online via PubMed here

An earlier version of the BOADICEA model is described in the following papers:

Antoniou, A.C., Pharoah, P.P.D., Smith, P. & Easton, D.F. 2004. The BOADICEA model of genetic susceptibility to breast and ovarian cancer, *British Journal of Cancer*, **91**(8), 1580–1590.

Available online here

Antoniou, A.C. and Easton, D.F. 2006. Risk prediction models for familial breast cancer, *Future Oncology*, **2**(2), 257–274.

Available online via PubMed here

Antoniou A.C., Durocher F., Smith P., Simard J., INHERIT BRCAs program members and Easton D. 2006. BRCA1 and BRCA2 mutation predictions using the BOADICEA and BRCAPRO models and penetrance estimation in high-risk French-Canadian families, *Breast Cancer Research*, **8**(R3), doi:10.1186/bcr1365.

Available online here

Barcenas C.H., Hosain G.M.M., Arun B., Zong J.H., Zhou X.J., Chen J.F., Cortada J.M., Mills G.B., Tomlinson G.E., Miller A.R., Strong L.C. and Amos C.I. 2006. Assessing BRCA carrier probabilities in extended families, *Journal of Clinical Oncology*, **24**(3), 354–360.

Available online here

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# 1. INTRODUCTION

The BOADICEA Web Application (BWA) enables you to estimate BRCA mutation carrier probabilities and breast/ovarian cancer risks on the basis of family history. This document provides a brief introduction to its use. We strongly recommend that new users read these notes before attempting to use this software.

This guide accompanies BWA version 3.0.

In this guide, key points are marked with an arrowhead ►. These short paragraphs highlight the most important issues. Additional information is available in the Frequently Asked Questions section of the BOADICEA Web site.

## 1.1 Computer requirements

The BWA is designed for use with modern Web browsers such as *Google Chrome* and *Mozilla Firefox*. However, you may need to make some adjustments to your browser settings to enable the program to work properly.

**► The BWA uses scripts that run in your browser to check input data, and so your browser must have 'active scripting' enabled (it is quite likely to be enabled already).**

**► The BWA displays pedigree drawings and graphs of breast/ovarian cancer risks in popup windows. Some browsers will prompt you to 'Allow popup windows from this site?' If you OK this, then the program should function normally.**

## 1.2 Web page submission

The BWA processes Web pages in a predetermined order. As a result, there are some constraints on Web page submission:

**► The program will not process 'cached' Web pages accessed by pressing the 'Back' arrow in your browser. If the program detects an incoming cached Web page, it will generate an error message and restore the session to its previous state.**

**► Always use the buttons at the bottom of each Web page to submit it for processing, rather than the 'Return' key on your keyboard. Also, try to avoid pressing the submit button several times if the program fails to respond right away.**

**► At any point, you can reinitialise your session by pressing the 'Reset' button, or terminate it by pressing the 'Logout' button. If you press 'Reset', the program will reset the session without logging you out. In both cases, all data files created on the Web server up to that point will be deleted.**

## 1.3 BOADICEA workflow

The BWA program has been designed to accommodate online and batch processing workflows (Figure 1). The online processing workflow enables you to build a new pedigree data set online, and to edit to process it. The batch processing workflow enables you to upload a BOADICEA import/export (I/E) format data file containing multiple pedigree data sets and to initiate batch jobs to validate and process them one after another. Multiple pedigree data sets submitted for batch processing cannot be edited before processing.

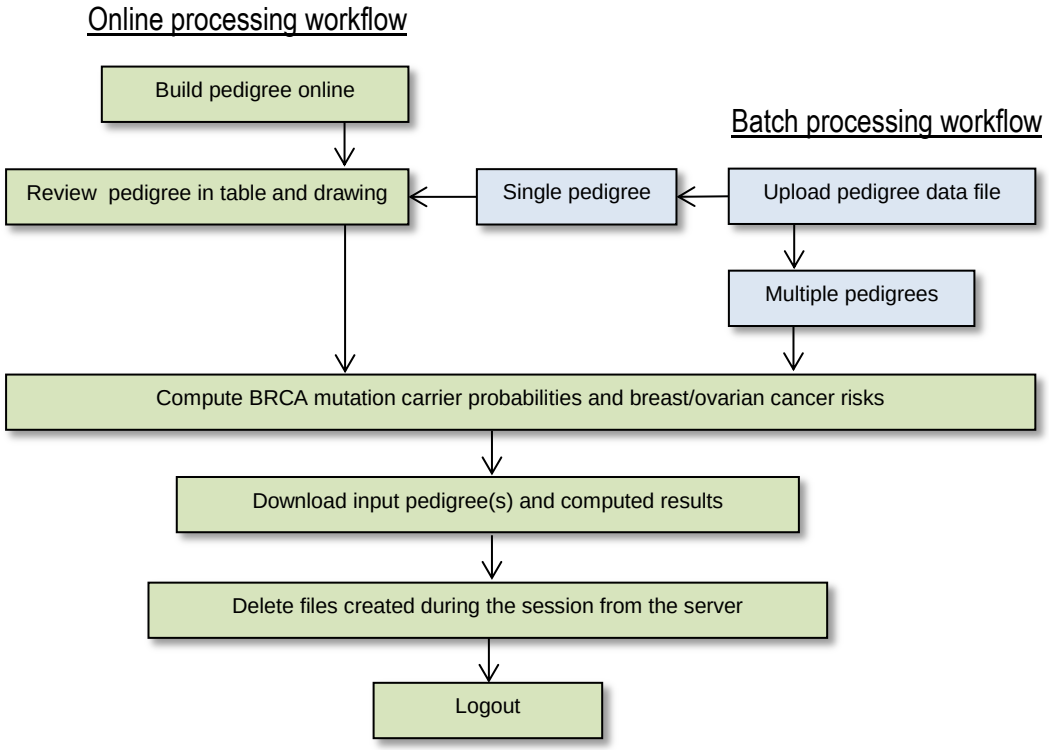

Online processing workflow
Build pedigree online
Batch processing workflow
Review pedigree in table and drawing
Single pedigree
Upload pedigree data file
Multiple pedigrees
Compute BRCA mutation carrier probabilities and breast/ovarian cancer risks
Download input pedigree(s) and computed results
Delete files created during the session from the server
Logout

**Figure 1. The BWA workflows. The online processing workflow (shaded green) enables you to build a pedigree data set online, and to edit and process it. The batch processing workflow (initial steps shaded blue) enables you to upload a BOADICEA I/E format data file containing multiple pedigree data sets and to initiate batch jobs to validate and process them one after another. If you upload a text file that contains a single pedigree data set, the program will assume that the pedigree was built online, so that you can edit it before processing.**

The BWA online processing workflow consists of the following main activities:

- Creating the pedigree data set
- Validating the pedigree data set
- Reviewing the pedigree data set
- Adjusting model parameters
- Computing risks
- Interpreting results
- Saving results

These activities are described in sections 2 to 8 of this guide.

The BWA batch processing workflow consists of the following main activities:

- Uploading the pedigree data sets
- Validating the pedigree data sets
- Computing risks
- Saving results

These activities are described in section 9 of this guide.

# 2. CREATING YOUR PEDIGREE

Once you have logged in, the BWA generates a SESSION OPTION Web page (Figure 2).

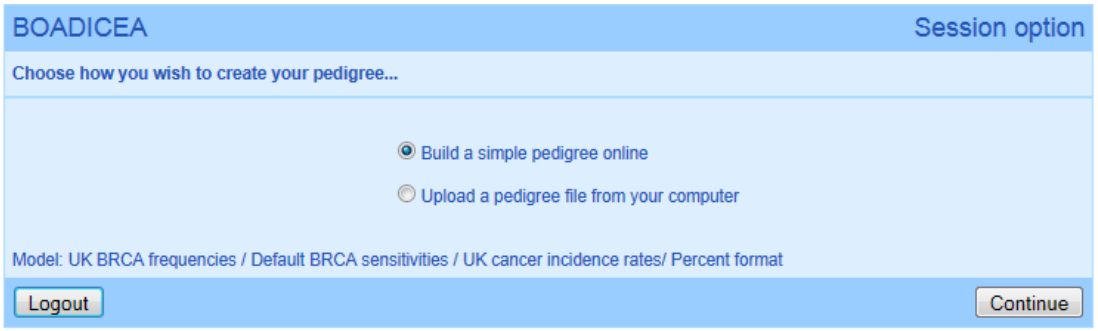

BOADICEA
Session option
Choose how you wish to create your pedigree...
Build a simple pedigree online
Upload a pedigree file from your computer
Model: UK BRCA frequencies / Default BRCA sensitivities / UK cancer incidence rates/ Percent format
Logout
Continue

**Figure 2. The SESSION OPTION Web page.**

The SESSION OPTION Web page (Figure 2) prompts you to choose how you wish to input your pedigree data set(s):

- Build a simple pedigree online
- Upload a pedigree file from your computer

If you choose to upload a BOADICEA I/E format data file from your computer, the file can contain a single pedigree data set or multiple pedigree data sets. Select the appropriate option and press 'Continue' to submit your request for processing. The 'Model' entry in the bottom left-hand corner of the SESSION OPTION Web page (Figure 2) describes the default BOADICEA model parameter settings (described in section 4 of this guide).

**► Pedigree data sets can include a maximum of 275 family members.**

## 2.1 Building your pedigree online

The BWA enables you to build and edit simple pedigrees online (sample shown in Figure 3).

**► Pedigrees built online must have simple structures: loops and consanguineous relationships are not allowed (see section 2.2 'Uploading pedigrees' for instructions on processing pedigrees with these more complex relationships).**

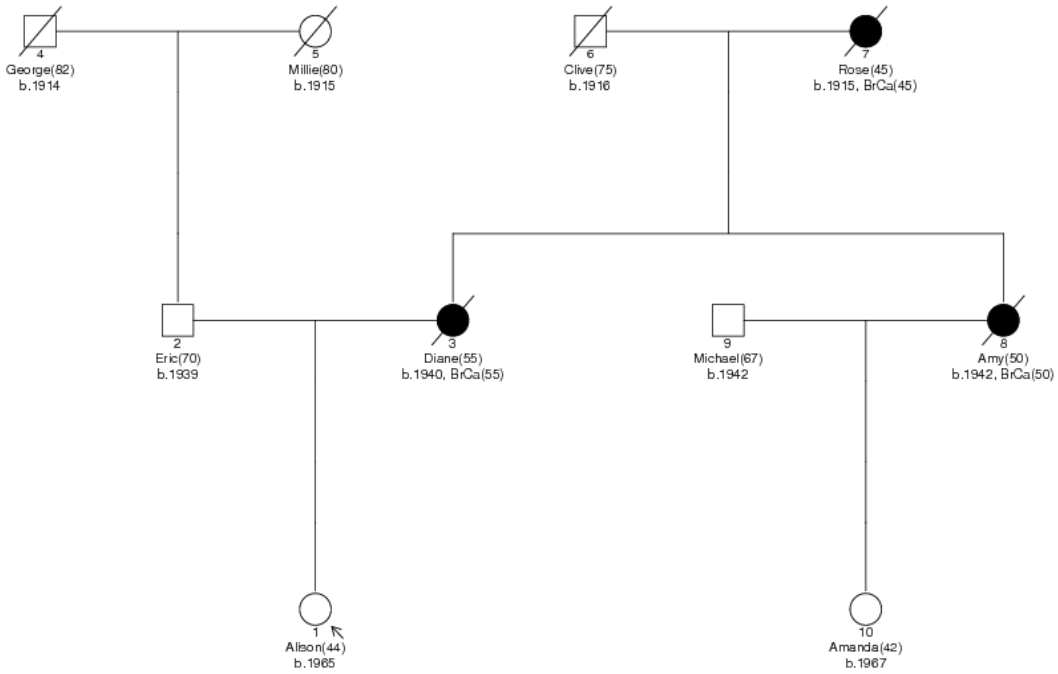



**Figure 3. Sample pedigree built online with the BWA. The pedigree is annotated in the conventional manner: the target (index or subject of the risk calculation) is marked with an arrow, and individuals who have developed cancer are shaded.**

If you choose to build a pedigree data set online, the program will first generate a PEDIGREE NUMBER Web page which prompts for a unique pedigree identifier. It will then generate a series of Web pages to enable you to input your family history data.

Online pedigree building is a two stage process:

- Build the 'core' family
- Add additional family members

These activities are described below.

## 2.1.1 Building the core family

When you build a pedigree online, you must first build the 'core family' which consists of the consultand and her parents. The BWA program generates CONSULTAND (Figure 4), MOTHER OF CONSULTAND and FATHER OF CONSULTAND Web pages to enable you to do this.

At first sight, CONSULTAND Web pages (Figure 4) appear quite complicated. However, they have been designed to enable you to input data quickly and easily.

The CONSULTAND Web page has two tabbed sections labelled 'Clinical history' (shown in Figure 4a) and 'Breast cancer pathology' (shown in Figure 4b). You can access either section by clicking on the corresponding tab in the top left-hand corner of the Web page.

**► The consultand can be specified as alive or dead - this option has been included to make retrospective pedigree data entry easier.**

## Clinical history

You can use the 'Clinical history' section (Figure 4a) to enter details of a family member's sex, vital status, age or age at death (age at last follow up), cancer history and genetic status.

## Breast cancer pathology

Similarly, you can use the 'Breast cancer pathology' section to enter details a family member's breast cancer pathology results.

**► In order to input breast cancer pathology data, you must first ensure that the family member has a breast cancer diagnosis is specified in the 'Clinical history' section.**

The 'Breast cancer pathology' section prompts for the status of the following pathology parameters:

- Estrogen Receptor (ER)
- Progestrogen Receptor (PR)
- Human Epidermal Growth Factor Receptor Two (HER2)
- Cytokeratin Fourteen (CK14)
- Cytokeratin Five/Six (CK5/6)

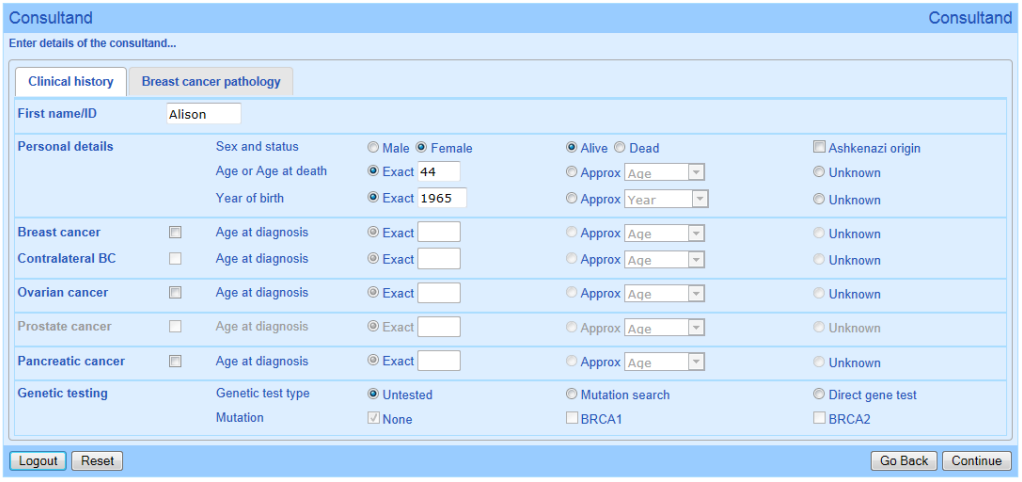
Only certain combinations of pathology parameters are permitted. When you input pathology data, the program enables/disables the pathology input devices in accordance with the following rules:

- ER status must be specified as 'positive' or 'negative'
- PR and HER status can only be specified for ER 'negative' family members
- CK14 and CK5/6 status can only be specified for triple negative* family members

*Triple negative family members are ER negative, PR negative and HER2 negative.

Work down the 'Clinical history' and 'Breast cancer pathology' sections of the Web page entering the details for the consultand, and then press ‘Continue’ to submit it for processing. The MOTHER OF CONSULTAND and FATHER OF CONSULTAND Web pages that follow have the same format.

(a)




(b)

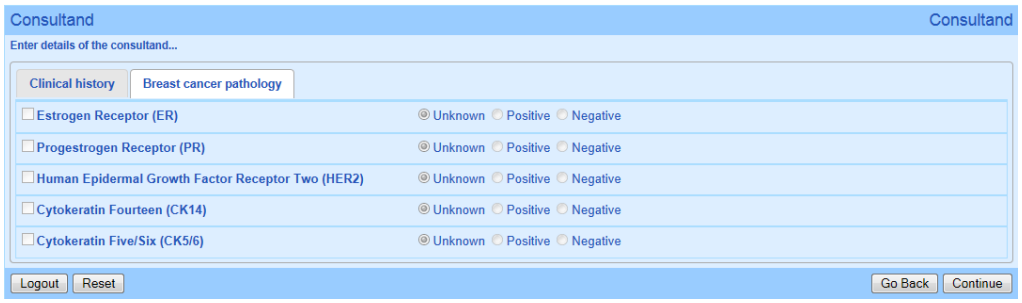



**Figure 4. The CONSULTAND Web page. This Web page is used to capture details of the first family member. By default, the BWA assumes that the consultand is also the target (index or subject of the risk calculation). (a) The CLINICAL HISTORY section of the Web page. (b) The BREAST CANCER PATHOLOGY section of the Web page.**

## Mandatory data items

The CONSULTAND Web page (Figure 4) shows the data parameters that are recorded for all family members. Most of these parameters are optional. However, a few key parameters are mandatory:

- All family members must have 'First name/ID' specified
- All family members must have an 'Age or age at death' and 'Year of birth' specified, even if this option is set to 'Unknown'
- The consultand must have 'Age or age at death' and 'Year of birth' specified

The ‘First name/ID’ is used solely to identify family members in data tables and pedigree drawings. When a CONSULTAND Web page is generated for the first time, the ‘First name/ID’ text field is initialised with ‘Anon’ for anonymous. To update the ‘First name/ID’, left click the text box to clear it, and enter your own identifier. The ‘Age or age at death’ is the age at last follow-up.

### Setting the current age from year of birth

If the family member is alive, you can set his/her current age from the year of birth (or vice versa). To do this, type a year into the ‘Year of birth’ text field, and click the ‘Age or age at death’ radio button. The current age will then appear in the adjacent text field.

### Mandatory data items for family members with cancer

All family members with cancer must have the following parameters specified to avoid underestimating risks:

- ‘Age or age at death’
- ‘Year of birth’
- ‘Age at diagnosis’

**► If you specify an age at cancer diagnosis as ‘Unknown’, the program will set it equal to the ‘Age or age at death’ when risks are computed.**

**► If you specify an ‘unknown’ age at diagnosis with the ‘AU’ code in a BOADICEA I/E format pedigree file (see Appendix A for format description), the program will set it equal to the ‘Age or age at death’ when the file is uploaded for processing.**

### Family members without cancer

Family members without cancer must have the following parameters specified in order to be included in the BOADICEA risk calculation:

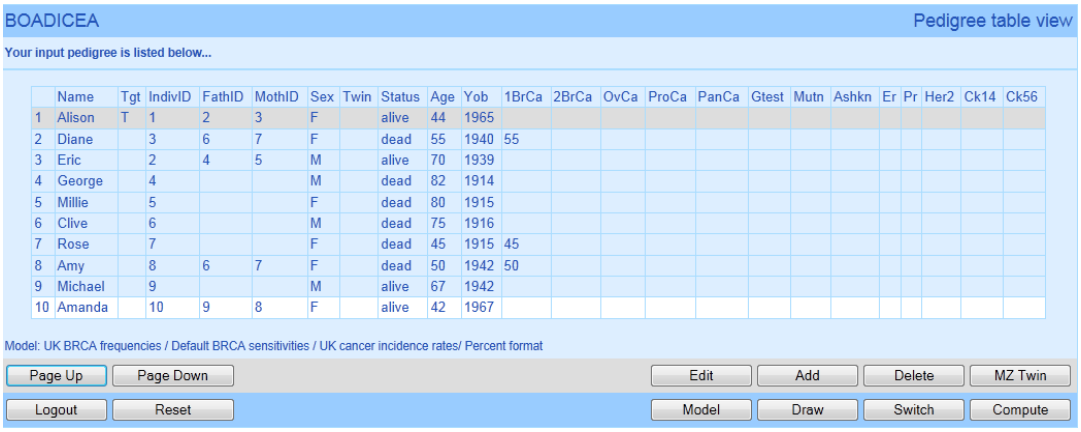
- ‘Age or age at death’
- ‘Year of birth’

### Family members without data

If you need to add a family member for whom no data exist, you can specify the ‘First name/ID’ as ‘Anon’, the ‘Age or age at death’ as ‘Unknown’ and the 'Year of birth' as 'Unknown', and then submit the Web page for processing.

## 2.1.2 Adding additional family members

Once you have input details of the core family members, the program will generate a PEDIGREE TABLE VIEW Web page (Figure 5) listing these three individuals.




| | Name | Tgt | IndivID | FathID | MothID | Sex | Twin | Status | Age | Yob | 1BrCa | 2BrCa | OvCa | ProCa | PanCa | Gtest | Mutn | Ashkn | Er | Pr | Her2 | Ck14 | Ck56 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Alison | T | 1 | 2 | 3 | F | | alive | 44 | 1965 | | | | | | | | | | | | | |
| 2 | Diane | | 3 | 6 | 7 | F | | dead | 55 | 1940 | 55 | | | | | | | | | | | | |
| 3 | Eric | | 2 | 4 | 5 | M | | alive | 70 | 1939 | | | | | | | | | | | | | |
| 4 | George | | 4 | | | M | | dead | 82 | 1914 | | | | | | | | | | | | | |
| 5 | Millie | | 5 | | | F | | dead | 80 | 1915 | | | | | | | | | | | | | |
| 6 | Clive | | 6 | | | M | | dead | 75 | 1916 | | | | | | | | | | | | | |
| 7 | Rose | | 7 | | | F | | dead | 45 | 1915 | 45 | | | | | | | | | | | | |
| 8 | Amy | | 8 | 6 | 7 | F | | dead | 50 | 1942 | 50 | | | | | | | | | | | | |
| 9 | Michael | | 9 | | | M | | alive | 67 | 1942 | | | | | | | | | | | | | |
| 10 | Amanda | | 10 | 9 | 8 | F | | alive | 42 | 1967 | | | | | | | | | | | | | |

**Figure 5. The PEDIGREE TABLE VIEW Web page. This Web page displays the input pedigree as a tabulated data set. It includes two sets of function buttons: the top row of buttons (highlighted in grey) are used to navigate and edit the pedigree; the bottom row of buttons (highlighted in blue) include functions to manage the login session, update BOADICEA model parameters, draw the pedigree, switch the target (index or subject of the risk calculation) and compute risks.**

The PEDIGREE TABLE VIEW Web page also includes a set of editing function buttons (grey table row, Figure 5) that are used to navigate the pedigree and to extend it further. These functions are described below.

### Scrolling the pedigree table

The PEDIGREE TABLE VIEW Web page (Figure 5) displays up to ten table rows at a time. Press the 'Page Up' function button (bottom left-hand corner, Figure 5) to scroll up through your pedigree table (and vice versa).

### Editing family member details

You can view and update details of any family member using the 'Edit' function (top row of function buttons, Figure 5). To do this, first select the individual from the PEDIGREE TABLE VIEW Web page (Figure 5) by left clicking the appropriate table row. When you do this, the table row will be highlighted in white to confirm your selection. Then press the 'Edit' function button to retrieve the data for that individual. Once you have submitted your request, the program will return the requested data in an EDIT DETAILS Web page. The EDIT DETAILS Web page has exactly the same format as the CONSULTAND Web page (Figure 4) and functions in the same way. You can then view and update the requested data, and resubmit it for processing. Once you have resubmitted the EDIT DETAILS Web page, the PEDIGREE TABLE VIEW Web page will be displayed once more with the updated data.

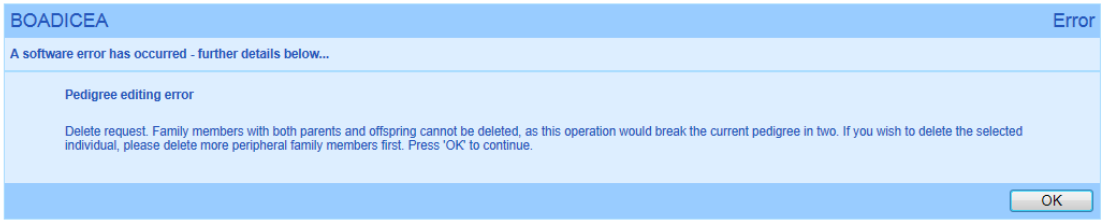

BOADICEA
Error
A software error has occurred - further details below...
Pedigree editing error
Delete request. Family members with both parents and offspring cannot be deleted, as this operation would break the current pedigree in two. If you wish to delete the selected individual, please delete more peripheral family members first. Press 'OK' to continue.
OK

**Figure 6. An ERROR Web page describing a 'Pedigree editing error'. These Web pages are returned when the program detects an inconsistency in your pedigree data set.**

When you submit an EDIT DETAILS Web page for processing, the program will amend the pedigree data set and then check it for data errors and inconsistencies. If the program finds an error in the updated data set, it will return an ERROR Web page describing the problem (Figure 6). If an error is detected, the program will cancel the requested operation and restore the pedigree as it was before you attempted to update it.

## Adding family members

You can add additional family members using the 'Add' function (top row of function buttons, Figure 5). You can extend the pedigree by selecting an existing family member, and then adding one of the following:

- Parents
- A partner and offspring
- One or more siblings

To extend the pedigree, you must first identify the branch of the pedigree that you wish to extend by selecting an existing family member (left click the relevant table row as before). When you do this, the table row will be highlighted in white to confirm your selection. Then press the 'Add' function button (Figure 5) to generate an ADD NEW FAMILY MEMBER Web page (Figure 7).

**Figure 7. The ADD NEW FAMILY MEMBER Web page.**

The ADD NEW FAMILY MEMBER Web page shows four options:

- Add parents
- Add a partner and offspring
- Add sibling(s)
- Return to PEDIGREE TABLE VIEW

The family member that you have just selected may or may not have parents included in the pedigree. As a result, when the program generates an ADD NEW FAMILY MEMBER Web page, it disables either the 'Add parents' or 'Add a new sibling' option because:

- If parents exist already in a nuclear family, you cannot add them
- If parents are missing from a nuclear family, you cannot add siblings*

*All family members must be physically connected. In a nuclear family, parents provide the physical connection between siblings.

Choose your preferred option on the ADD NEW FAMILY MEMBER Web page and press 'Continue' to submit your request for processing.

*Adding parents*

If you select the 'Add parents' option, the program will generate ADD FATHER and ADD MOTHER Web pages to enable you to add these new family members.

*Adding a partner and offspring*

If you select the 'Add a partner and offspring' option, the program will generate ADD NEW PARTNER and ADD OFFSPRING Web pages to enable you to add these new family members.

*Adding siblings*

To add one or more siblings, you must first select the ‘Add a new sibling’ option, and then use the 'No.' selection list to specify the number of siblings that you wish to add (up to five at a time). The program will then generate the corresponding number of ADD SIBLING Web pages to enable you to add these additional relatives.

The ADD FATHER, ADD MOTHER, ADD PARTNER, ADD OFFSPRING and ADD SIBLING Web pages have exactly the same format as the CONSULTAND Web page (Figure 4). As soon as you have input these additional data, the program will return an updated PEDIGREE TABLE VIEW Web page.

**► New family members are added to the end of the pedigree table so you may have to scroll down the table in the PEDIGREE TABLE VIEW Web page to see them.**

*Adding aunts, uncles and cousins*

Once you have built the core family, you may wish to add aunts, uncles and cousins. This is straightforward. However, you do need to be aware of the following pedigree building issue: in order to add (for example) a maternal aunt, you must first add maternal grandparents. You must do this because the maternal grandparents provide the physical link in the pedigree between the target's mother and maternal aunt.

To add a maternal aunt, first add maternal grandparents by selecting the target's mother, and then use the 'Add' function to access the ADD NEW FAMILY MEMBER Web page (Figure 7). You can then use the 'Add parents' option to add the target's maternal grandparents. If you have no information on the maternal grandparents, you can still add them to the pedigree by specifying the 'First name/ID' as 'Anon', and the 'Age or age at death' as 'Unknown' for both individuals. That way, they will be included in the pedigree, but they will make no contribution to the calculated risks.

Once you have added the maternal grandparents, select the target's mother again, and use the 'Add' function to access the ADD NEW FAMILY MEMBER Web page (Figure 7), and then use the 'Add a new sibling' option to add the mother's sister (i.e. the target's maternal aunt).

Once you have added the target's maternal aunt, you can then add a maternal cousin. To do this, select the target's maternal aunt and use the 'Add' function to access the ADD NEW FAMILY MEMBER Web page (Figure 7), and then use the 'Add a partner and offspring' option to add a new maternal uncle and child (i.e. the target's maternal cousin). As before, if you have no information on the maternal uncle, you can still add this person to the pedigree by specifying the 'First name/ID' as 'Anon', and the 'Age or age at death' as 'Unknown'.

## Deleting family members

You can delete existing family members using the ‘Delete’ function (top row of function buttons, Figure 5). To do this, select the individual that you want to delete

(left click the relevant table row as before), and press the 'Delete' button to submit your request. When you do this, the program will first check the structure of your pedigree to ensure that the individual can be safely deleted.

**► The program will not allow a deletion that will break the pedigree into two separate trees. As a result, you can only delete founders and un-partnered offspring**.

**► If you delete the last remaining child in a nuclear family where an outlying parent (sometimes termed a 'marry-in') is connected to the pedigree solely via his/her partner then both the child and the outlying parent will be deleted.**

**► Pedigrees must have a minimum of three family members. As a result, deletions are not permitted when you have reached this limit.**

If the program determines that the requested operation will break the pedigree into two separate trees, it will return an ERROR Web page (Figure 6) describing the problem. Otherwise, the selected individual will be deleted and the program will return an updated PEDIGREE TABLE VIEW Web page (Figure 5).

## 2.2 Uploading your pedigree

The program enables you to build simple pedigrees online. However, at present, these pedigree structures cannot include loops or consanguineous relationships. As a result, the program also provides an 'Upload' function to enable you to process more complex pedigrees. This module can also be used to process pedigrees exported from third party software packages such as Clinical Pedigree, Progeny or PED6.

**► Please note: we are unable to offer any guarantees or support for third party software.**

To do this, you must first prepare a text file in the BOADICEA I/E file format (see Appendix A). If your pedigree data are stored in a database, BOADICEA I/E pedigree files can be created by setting up a database query to export the parameters in a TAB delimited text format. Alternatively, BOADICEA I/E files can be created directly in *Microsoft Excel* (see Appendix B).

To upload a BOADICEA I/E pedigree file for processing, select 'Upload a pedigree file from your computer' on the SESSION OPTION Web page (Figure 2), and press 'Continue' to submit your request for processing. The program will then generate a PEDIGREE FILE UPLOAD Web page (Figure 8).

**Figure 8. The PEDIGREE FILE UPLOAD Web page.**

The PEDIGREE FILE UPLOAD Web page (Figure 8) enables you to select a text file on your computer for processing. Press the 'Browse…' button to generate a further FILE NAVIGATION window (Figure 9), and use this to select a BOADICEA I/E format pedigree file from your system for processing.

**► For security reasons, the program checks the names of text files uploaded to the server for processing. As a result, it may display an error message when you press the 'Upload File' button. The pedigree file name must include a three letter extension (e.g. 'pedigree.txt' or 'pd4556.dat'). If the error message persists, try copying the pedigree file onto the C: drive of your computer, and reloading it from there.**

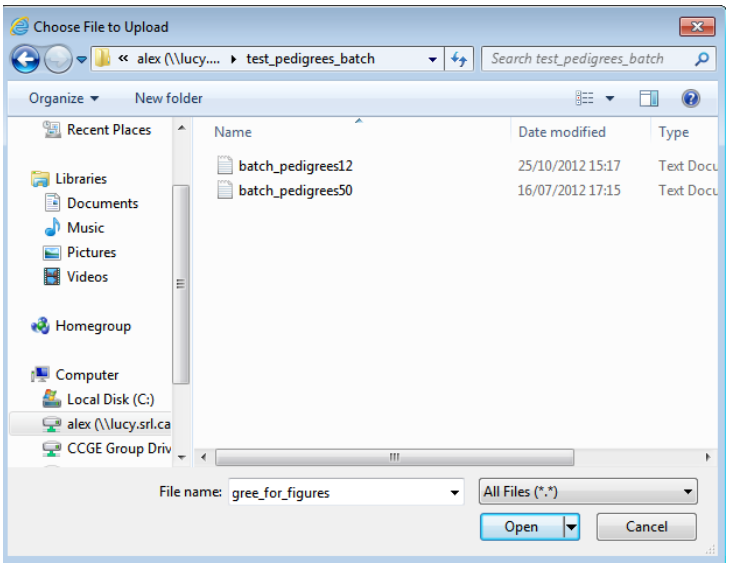



**Figure 9. The FILE NAVIGATION window.**

## Processing a single pedigree data set

The BOADICEA I/E text file that you upload for processing can contain a single pedigree data set or multiple pedigree data sets. When you upload the file, the program first runs a check to see how many pedigree data sets are included within it. If the file contains a single pedigree data set, the program will then validate it i.e. run checks for data errors and inconsistencies. If the pedigree data set fails validation, the program will generate an ERROR Web page (Figure 6) describing the problem. If this

happens, you will have to amend the pedigree file before you can proceed further (see Appendix B for information on editing BOADICEA I/E pedigree files in *Microsoft Excel*). Alternatively, if the pedigree data set passes validation, the program will return a PEDIGREE TABLE VIEW Web page (Figure 5) listing the first ten family members.

**Processing multiple pedigree data sets**

If the BOADICEA I/E file contains multiple pedigree data sets, the program will switch to the 'batch processing workflow' to initiate batch jobs to validate and process each pedigree data set (see section 9 of this guide for more details).

**Editing uploaded pedigrees**

Once you have uploaded a pedigree data set, you can edit and extend it online as normal using the PEDIGREE TABLE VIEW functions (described in section 2.1.2).

## 2.3 Specifying monozygotic twins

The BWA program includes functions to select/deselect monozygotic (MZ) twins in your pedigree.

**► In order for siblings to be considered eligible for MZ twinning, they must have the same year of birth, sex, age (if both living) and genetic test results. These data must be consistent for siblings to appear in the list of potential MZ twins.**

**► You can twin siblings where one individual has had a genetic test. If both siblings have had a genetic test (rare in practice), the genetic test results must be compatible.**

**► The program only allows you to set MZ twins: MZ triplets and quadruplets are not allowed (these are rare in practice). You can identify up to 10 pairs of MZ twins in a BOADICEA pedigree.**

Once your pedigree is displayed in the PEDIGREE TABLE VIEW Web page (Figure 5), you can identify siblings for twinning purposes using the 'MZ twin' function (top row of function buttons, Figure 5). To do this, press the 'MZ Twin' button. The program will then search your pedigree for:

- Pairs of siblings that have not been specified as MZ twins but could be
- Existing MZ twins

**► Searching large pedigrees for MZ twins can be time consuming.**

When the search is complete, the program will return a TWIN FAMILY MEMBERS Web page (Figure 10) which enables you to select or deselect MZ twins.

**Figure 10. The TWIN FAMILY MEMBERS Web page.**

The 'Select MZ twins' menu (Figure 10) lists all pairs of siblings that have not been specified as MZ twins but could be. To select a new pair of MZ twins, choose the appropriate sibling pair from this list and press 'Continue' to submit your request for processing. The program will then update your pedigree and return a PEDIGREE TABLE VIEW Web page. The new MZ twins will be identified in the pedigree table with unique identifiers in the 'Twin' data column (Figure 5).

The 'Deselect MZ twins' menu (Figure 10) lists the existing MZ twin pairs. To deselect existing MZ twins, choose the MZ twins from this list and press 'Continue' to submit your request for processing. The program will then deselect the MZ twins (i.e. remove their MZ twin status) and return a PEDIGREE TABLE VIEW Web page.

### 2.3.1 Identifying monozygotic twins in BOADICEA import/export pedigree files

When you upload a BOADICEA I/E pedigree file for processing, you can identify MZ twins using the 'Twin' data item in column 8 (described in Appendix A).

**► In BOADICEA I/E pedigree files, you can identify monozygotic twins by setting the 'Twin' data item to any one of the following characters: 1 2 3 4 5 6 7 8 9 A**

## 2.4 Ashkenazi Jewish pedigrees

The BWA program includes facilities for identifying Ashkenazi Jewish pedigrees. If you identify an input pedigree as an Ashkenazi Jewish pedigree, the program will adjust the BOADICEA model parameters (described in section 4 of this guide) to ensure that appropriate mutation frequencies are set prior to your risk calculation. Additional information on processing Ashkenazi Jewish pedigrees is available in the Frequently Asked Questions section of the BOADICEA Web site.

### 2.4.1 Building Ashkenazi Jewish pedigrees online

When you build a pedigree online, you can identify an Ashkenazi Jewish family by selecting the 'Ashkenazi origin' checkbox on the CONSULTAND Web page (Figure 4).

**► When you build pedigrees online, the 'Ashkenazi origin' checkbox is only enabled on the CONSULTAND Web page as the program only requires you to supply this information once.**

### 2.4.2 Editing Ashkenazi Jewish pedigrees

When you edit pedigrees online using the functions on the PEDIGREE TABLE VIEW Web page (Figure 5), you can identify an Ashkenazi Jewish family by selecting 'Ashkenazi' BRCA mutation frequencies with the 'Model Parameters' module (see section 4 of this guide for more details).

When pedigrees are edited online, Ashkenazi Jewish model parameters can only be selected (or deselected) using the 'Model Parameters' module. Although EDIT DETAILS Web pages (used to edit details of a chosen family member) include an 'Ashkenazi origin' checkbox, you will find that this checkbox always disabled. This ensures that Ashkenazi Jewish parameter settings remain consistent in the pedigree data and model data files stored on the server.

When you select 'Ashkenazi' BRCA mutation frequencies with the 'Model Parameters' module, the current target (index or subject of the risk calculation) will then be flagged as an Ashkenazi Jewish person in the PEDIGREE TABLE VIEW and EDIT DETAILS Web pages. In particular, the PEDIGREE TABLE VIEW Web page will show the letter 'A' in the target's 'Ashkn' data field, and the 'Ashkenazi origin' checkbox will be checked in the corresponding EDIT DETAILS Web page.

**► If you select Ashkenazi Jewish parameters with the 'Model Parameters' module, then the current target (index or subject of the risk calculation) will be identified as being of Ashkenazi Jewish origin.**

### 2.4.3 Uploading/downloading Ashkenazi Jewish pedigrees

When you upload a pedigree for processing, you can identify an Ashkenazi Jewish family by setting the 'Ashkn' data item (described in Appendix A) for one or more family members.

**► If you upload a pedigree that contains one or more Ashkenazi Jewish family members, the program will update the incoming data set so that only the target (index or subject of the risk calculation) is identified as being of Ashkenazi Jewish origin.**

**► If you download an Ashkenazi Jewish pedigree that has been processed online, then only the target (index or subject of the risk calculation) will be recognised as being of Ashkenazi origin in the downloaded data file.**

## 2.5 Pedigree validation

When you process a pedigree online, the BWA program runs tests to search for errors and inconsistencies in your input data. The tests will run at specific times during your session:

- When you build a pedigree online, the pedigree data set will be validated when you submit the FATHER OF PROBAND Web page for processing.

- When you upload a BOADICEA I/E data file for processing, the pedigree data set will be validated as soon as it is uploaded to the server.

- When you edit a pedigree online, the pedigree data will be validated after each edit operation. If the program determines that your requested modification will introduce an error in your pedigree data set, it will cancel the editing operation and restore the original pedigree as it was.

- Pedigrees are also validated before each BOADICEA risk calculation

If the pedigree data set passes validation, the session will continue as normal. Alternatively, if the pedigree data set fails validation, the program will generate an ERROR Web page describing the problem, and then restore the session as it was before the error occurred.

**► Pedigree validation helps to ensure that your pedigree data set is free of errors and internal inconsistencies. However, these checks are not comprehensive.**

**► Pedigree validation also checks that all family members are physically connected to the target (index or subject of the risk calculation) before the pedigree is processed.**

# 3. REVIEWING YOUR PEDIGREE

When pedigree data entry is complete, you can review your data before you proceed with a risk calculation. The PEDIGREE TABLE VIEW Web page (Figure 5) enables you to do this. The Frequently Asked Questions section of the BOADICEA Web site includes advice on important data issues.

## 3.1 Pedigree table

The PEDIGREE TABLE VIEW Web page (Figure 5) lists family members in a series of table rows. The corresponding column headings are explained in Table 1 below.

| Column Heading | Explanation |
|---|---|
| Name | First name/ID of the family member |
| Tgt | The target (index or subject of the risk calculation) |
| IndivID | The unique ID of the family member |
| FathID | The unique ID of the family member's father |
| MothID | The unique ID of the family member's mother |
| Sex | Male or female |
| Twin | Single characters used to identify identical twins |
| Status | Dead or alive |
| Age | Age or age at death (age at last follow up) |
| Yob | Year of birth |
| 1BrCA | Age at first breast cancer diagnosis |
| 2BrCa | Age at contralateral breast cancer diagnosis |
| OvCa | Age at ovarian cancer diagnosis |
| ProCa | Age at prostate cancer diagnosis |
| PanCa | Age at pancreatic cancer diagnosis |
| Gtest | Genetic test type. Mutation search (srch) or direct/predictive gene test (gtest) |
| Mutn | Genetic test result. Negative, BRCA1 +ve, BRCA2 +ve or BRCA1 and BRCA2 +ve |
| Ashkn | Ashkenazi origin |
| Er | Estrogen receptor status |
| Pr | Progestrogen receptor status |
| Her2 | Human epidermal growth factor receptor 2 status |
| Ck14 | Cytokeratin 14 status |
| Ck56 | Cytokeratin 5/6 status |

**Table 1. Column headings shown in the PEDIGREE TABLE VIEW Web page**

## 3.2 Pedigree drawing

The BWA also includes a module that you can use to draw your input pedigree using the Kinship package [*Zhao*, 2006]. To do this, press the 'Draw' button on the PEDIGREE TABLE VIEW Web page (Figure 5), and a pedigree drawing should appear in a popup window in a few seconds (Figure 11).

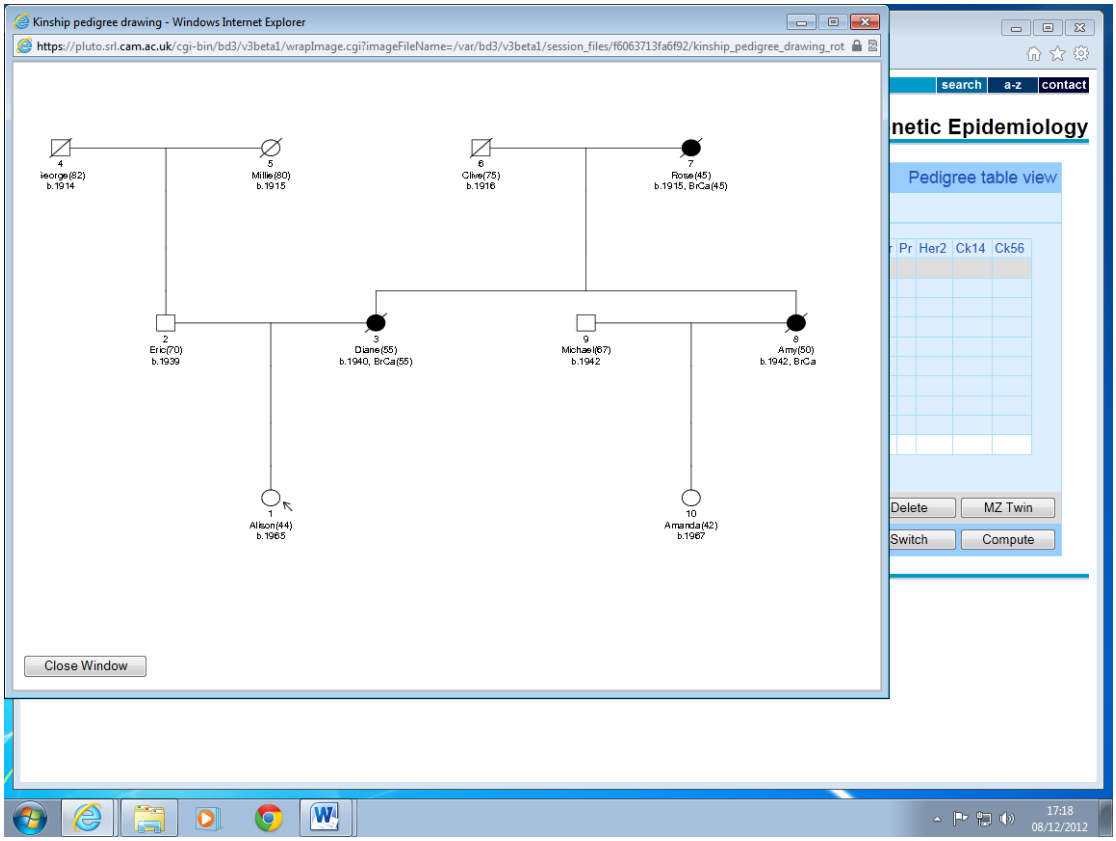



**Figure 11. Example pedigree drawing. Pedigree drawings are annotated in the conventional manner: the target (index or subject of the risk calculation) is identified with an arrow; family members who have developed cancer are shaded; unaffected family members are unshaded. The text annotation beneath each family member includes: a unique identifier, first name/ID and age at last follow up, year of birth, cancer history, genetic status and pathology status. If the family includes one or more Ashkenazi Jewish family members, the target will be annotated accordingly.**

**► In some cases, the Kinship package may fail to generate a pedigree drawing. If this happens, the pedigree drawing window will display an error message or will appear blank. However, this will not affect subsequent risk calculations.**

Additional information on pedigree drawing is available in the Frequently Asked Questions section of the BOADICEA Web site.

## 3.3 Switching the target

In PEDIGREE TABLE VIEW Web pages (Figure 5), the target (index or subject of the risk calculation) is identified with a grey table row and the letter 'T' in the 'Tgt' column. If you wish, you can change the target before you run your risk calculation. This enables you to compute risks for different family members. To do this, select the new target by left clicking the corresponding table row, and press the 'Switch' function button. If the selected individual has a valid year of birth and age at last follow up, the program will return an updated PEDIGREE TABLE VIEW Web page showing the new target individual.

**► The target of the risk calculation must have a valid year of birth and age at last follow up. If you select a family member as the new target who is lacking these details, the program will generate an error message and restore your pedigree to its original state.**

# 4. ADJUSTING MODEL PARAMETERS

The BWA program includes a 'Model Parameters' module that enables you to adjust BOADICEA model parameters for different populations. To view current model parameter settings, press the 'Model' button on the PEDIGREE TABLE VIEW Web page (Figure 5). The program will then return a MODEL PARAMETERS Web page (Figure 12).

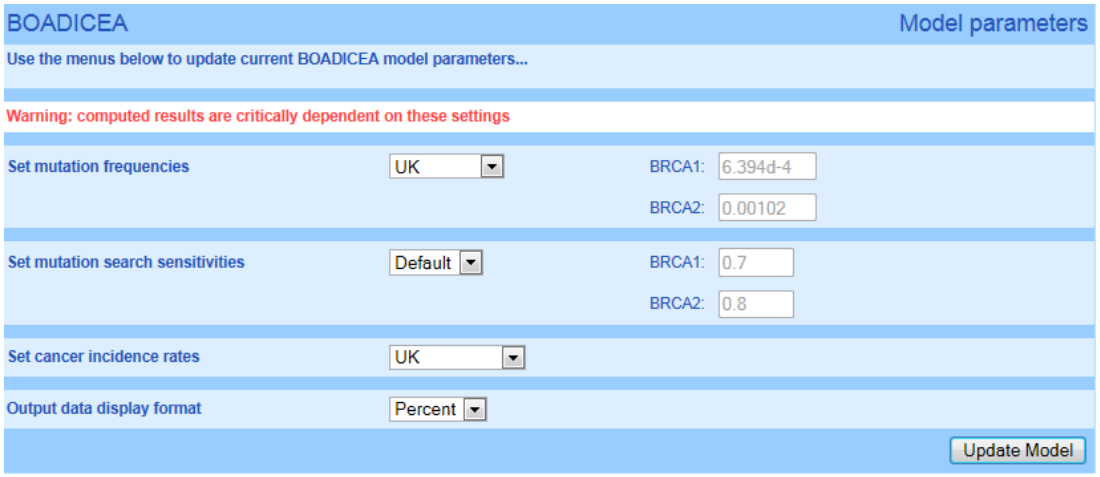



**Figure 12. The MODEL PARAMETERS Web page.**

The MODEL PARAMETERS Web page enables you to adjust six parameters:

- BRCA1 mutation frequency
- BRCA2 mutation frequency
- BRCA1 mutation search sensitivity
- BRCA2 mutation search sensitivity
- Cancer incidence rates
- Output data display format

You can reset any of these parameters before you run a BOADICEA risk calculation.

**► WARNING: computed results are critically dependent on the model parameter settings. If you are in any doubt about your model parameter settings, please contact us for further clarification (see the Contacts section of the BOADICEA Web site for more details) .**

**► When you login, the BWA program always sets 'UK' BRCA1 and BRCA2 mutation frequencies, 'Default' BRCA1 and BRCA2 mutation search sensitivities, UK cancer incidence rates, and the output data display format to 'Percent'.**

**► If you reset the current session by pressing either a 'Reset' or 'Next Pedigree' button, the program will restore 'UK' BRCA1 and BRCA2 mutation frequencies, 'Default' BRCA1 and BRCA2 mutation search sensitivities, UK cancer incidence rates, and the output data display format to Percent.**

## 4.1 BRCA mutation frequencies

The MODEL PARAMETERS Web page (Figure 12) shows the current BRCA1 and BRCA2 mutation frequencies in the upper two text boxes. To reset these parameters, select one of the three options on the 'Set mutation frequencies' selection list: 'UK', 'Ashkenazi', 'Iceland' or 'Custom'. If you select either the 'UK', 'Ashkenazi' or 'Iceland' option, appropriate preset mutation frequencies will appear in the adjacent text boxes. If you select the 'Custom' option, the program will clear and sensitise the adjacent text boxes, to enable you to input your own settings.

**► BRCA1 or BRCA2 mutation frequency is defined as the proportion of all BRCA1 or BRCA2 alleles in the population that is made of pathogenic mutations. It should not be confused with mutation *carrier* frequency which is a different quantity. For example, if p represents the mutation frequency in the population, the mutation carrier frequency is $p^2+2p(1-p)$. In this example, the BOADICA input should be "p".**

**► If you are uncertain how to specify BRCA1 and BRCA2 mutation frequencies, please contact us for further clarification.**

## 4.2 BRCA mutation search sensitivities

The MODEL PARAMETERS Web page (Figure 12) shows the current BRCA1 and BRCA2 mutation search sensitivities in the lower two text boxes. To reset these parameters, select one of the two options on the 'Set mutation search sensitivities' selection list: 'Default' or 'Custom'. If you select the 'Default' option, default mutation search sensitivities will appear in the adjacent text boxes. These default parameters were derived from UK data when the BOADICEA model was originally developed. If you select the 'Custom' option, the program will clear and sensitise the adjacent text boxes, to enable you to input your own settings.

**►BRCA1 and BRCA2 mutation search sensitivities define the proportion of BRCA1 and BRCA2 mutations that your mutation search is known to detect. They are expressed as decimal numbers in the range 0 to 1. For example, if you know that your mutation searches detect 90% of BRCA1 mutations, and 95% of BRCA2 mutations, you should input 0.9 and 0.95 in the corresponding text boxes on the MODEL PARAMETERS Web page.**

**► If you are uncertain how to specify BRCA1 and BRCA2 mutation search sensitivities, please contact us for further clarification.**

## 4.3 Cancer incidence rates

The MODEL PARAMETERS Web page (Figure 12) shows the cancer incidence rates in the third selection list. You can choose the cancer incidence rates to use in your risk calculation from the following options:

- UK
- UK-version-1
- Australia
- Canada
- USA-white

The 'UK' option specifies the most up-to-date UK cancer incidence rates. The 'UK-version-1' option specifies the UK cancer incidence rates used in previous versions of the BWA. We have included this option so that you can replicate results obtained with previous versions of the BWA program.

## 4.4 Output data display format

The MODEL PARAMETERS Web page (Figure 12) also shows the currently selected output data display format in the fourth selection list. You can specify the output data display format from the following options:

- Percent
- Decimal

If you select 'Percent' format, the program will display computed BRCA mutation carrier probabilities and breast/ovarian cancer risks as percentages e.g. a probability of 1 in 50 will be expressed as 2.0 percent.

If you select 'Decimal' format, the program will display computed BRCA mutation carrier probabilities and breast/ovarian cancer risks as decimal fractions with a value between zero and one e.g. a probability of 1 in 50 will be expressed as 0.020.

Additional information on model parameters is available in the Frequently Asked Questions section of the BOADICEA Web site.

# 5. COMPUTING RISKS

When you are satisfied that your input pedigree data and model parameters are correct, you can proceed with a BOADICEA risk calculation. To compute BRCA1 and BRCA2 mutation carrier probabilities and breast/ovarian cancer risks, press the 'Compute' button on the PEDIGREE TABLE VIEW Web page (Figure 5). The program will then run the risk calculation and return the results in a COMPUTED RESULTS Web page (Figure 13).

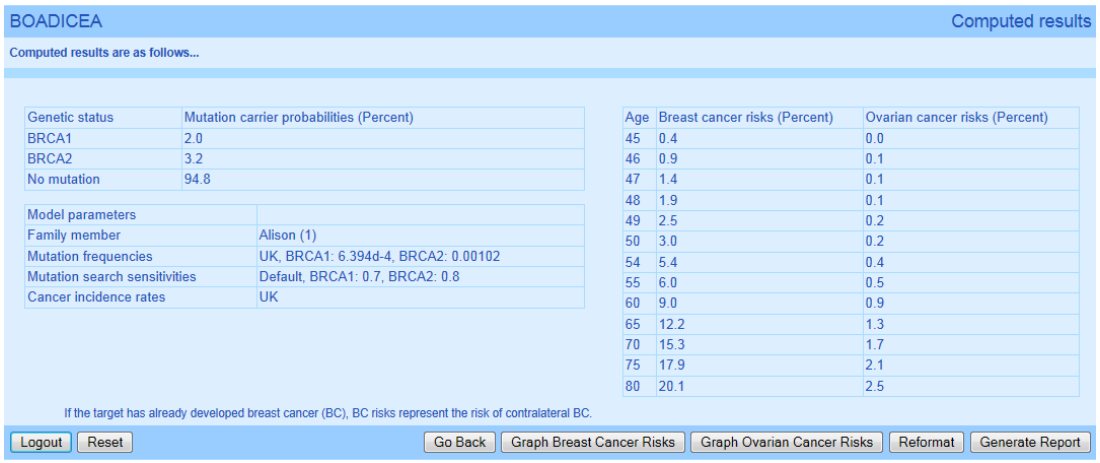



**Figure 13. The COMPUTED RESULTS Web page.**

The COMPUTED RESULTS Web page (Figure 13) displays the current model parameter settings and the results of your risk calculation: the top left-hand table lists BRCA1 and BRCA2 mutation carrier probabilities in either 'Percent' or 'Decimal' format; the bottom left-hand table lists the model parameter settings used in the risk calculation; and the right-hand table lists breast and ovarian cancer risks in either 'Percent' or 'Decimal' format.

## 5.1 Graphing breast cancer risks

The COMPUTED RESULTS Web page (Figure 13) displays computed BRCA mutation carrier probabilities and breast/ovarian cancer in data tables. However, you can also generate a graph of breast cancer risks plotted against the target's age. To do this, press the 'Graph Breast Cancer Risks' button on the COMPUTED RESULTS Web page (Figure 13), and a graph should appear in a popup window in a few seconds (Figure 14).

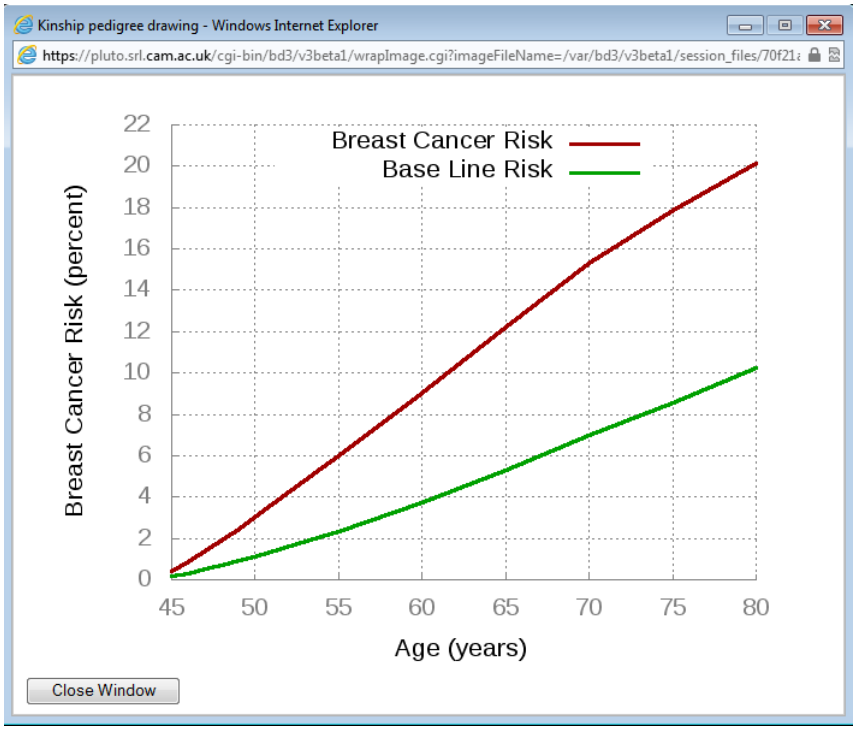



**Figure 14. Breast cancer risk graph. Breast cancer risks (expressed in percent) are plotted against age (expressed in years up to age 80). The red curve represents the target's breast cancer risk predicted by the BOADICEA model on the basis of the existing family history. The green curve represents the corresponding baseline breast cancer risks i.e. equivalent breast cancer risks predicted for a random individual in the general population.**

The breast cancer risk graph (Figure 14) shows two curves: (1) the red curve represents the target's breast cancer risks predicted by the BOADICEA model on the basis of the input pedigree data set; and (2) the green curve represents the corresponding baseline breast cancer risks i.e. the equivalent breast cancer risks predicted for a random individual in the general population.

The target's breast cancer risks predicted by the BOADICEA model (red curve, Figure 14) are computed using information for all family members in the input pedigree (for whom an 'Age or age at death' and 'Year of birth' have been specified).

Baseline breast cancer risks (green curve, Figure 14) are computed using only the following parameters for the target: sex, age at last follow up, year of birth and age at first breast cancer diagnosis (if applicable).

**► If the target has already developed one breast cancer, the breast cancer risks predicted by the BOADICEA model (red curve, Figure 14) represent the target's risk of contralateral breast cancer (as noted in the risk graph).**

**► Breast cancer risks are always expressed in percent in risk graphs.**

## 5.2 Graphing ovarian cancer risks

You can also generate a graph of ovarian cancer risks plotted against the target's age. To do this, press the 'Graph Ovarian Cancer Risks' button on the COMPUTED RESULTS Web page (Figure 13), and a graph should appear in a popup window in a few seconds (Figure 15).

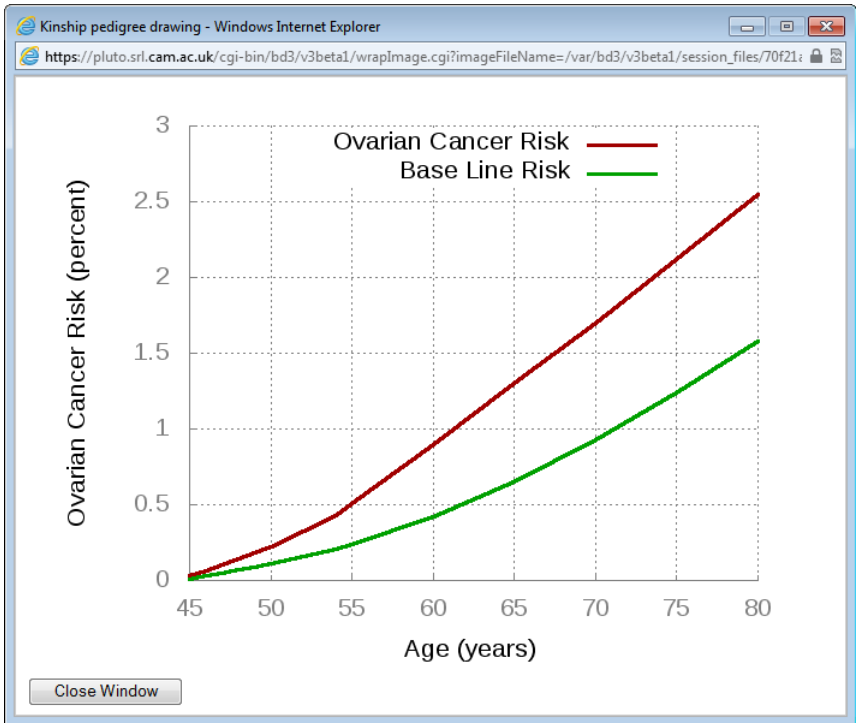



**Figure 15. Ovarian cancer risk graph. Ovarian cancer risks (expressed in percent) are plotted against age (expressed in years up to age 80). The red curve represents the target's ovarian cancer risk predicted by the BOADICEA model on the basis of the existing family history. The green curve represents the corresponding baseline ovarian cancer risks i.e. equivalent ovarian cancer risks predicted for a random individual in the general population.**

The ovarian cancer risk graph (Figure 15) shows two curves: (1) the red curve represents the target's ovarian cancer risks predicted by the BOADICEA model on the basis of the existing family history; and (2) the green curve represents the corresponding baseline ovarian cancer risks i.e. the equivalent ovarian cancer risks predicted for a random individual in the general population.

The target's ovarian cancer risks predicted by the BOADICEA model (red curve, Figure 15) are computed using information for all family members in the input pedigree (for whom an 'Age or age at death' and 'Year of birth' have been specified).

Baseline ovarian cancer risks (green curve, Figure 15) are computed using only the following parameters for the target: sex, age at last follow up, year of birth and age at first ovarian cancer diagnosis (if applicable).

**► Ovarian cancer risks are always expressed in percent in risk graphs.**

## 5.3 Changing the output data display format

By default, the BWA program displays BRCA mutation carrier probabilities and breast/ovarian cancer risks on the COMPUTED RESULTS Web page in 'Percent' format. However, you can change the output data display format from 'Percent' format to 'Decimal' format (and vice versa) by pressing the 'Reformat' button on the computed results Web page (Figure 13).

# 6. INTERPRETING RESULTS

The COMPUTED RESULTS Web page (Figure 13) lists the BRCA1 and BRCA2 mutation carrier probabilities and breast/ovarian cancer risks computed on the basis of your input pedigree.

## 6.1 BRCA mutation carrier probabilities

BRCA1 and BRCA2 mutation carrier probabilities are listed in the top left-hand table on the COMPUTED RESULTS Web page (Figure 13). These figures are conditional probabilities computed on the basis of the input pedigree data set and are expressed as follows:

If you selected 'Percent' format (as shown in Figure 13), the program will display computed BRCA mutation carrier probabilities as percentages e.g. a probability of 1 in 50 will be expressed as 2.0 percent.

If you selected 'Decimal' format, the program will display computed BRCA mutation carrier probabilities as decimal fractions with a value between zero and one e.g. a probability of 1 in 50 will be expressed as 0.020.

### 6.1.1 Family members who carry both BRCA1 and BRCA2 mutations

For modelling purposes, the BWA program assumes that family members who carry both BRCA1 and BRCA2 mutations are BRCA1 positive only. This assumption has an important implication when interpreting results:

**► If the target (index or subject of the risk calculation) has tested positive for both BRCA1 and BRCA2 mutations, she/he will be assigned a BRCA1 mutation carrier probability of 1.0 only.**

## 6.2 Breast and ovarian cancer risks

Breast and ovarian cancer risks are listed in the right-hand table of the COMPUTED RESULTS Web page (Figure 13). Risks are computed for the target (the index or subject of the risk calculation) at one year intervals for the next five years, and then at ages divisible by five years up to age 80. In addition, the 10-year breast/ovarian cancer risks are also included.

These figures are conditional probabilities computed on the basis of the input pedigree data set and are expressed as follows:

If you selected 'Percent' format (as shown in Figure 13), the program will display breast/ovarian cancer risks as percentages e.g. a risk of 1 in 50 will be expressed as 2.0 percent.

If you selected 'Decimal' format, the program will display breast/ovarian cancer risks as decimal fractions with a value between zero and one e.g. a risk of 1 in 50 will be expressed as 0.020.

**► Cancer risks will only be computed if the target (index or subject of the risk calculation) is a female unaffected by cancer, or a female who has developed one breast cancer.**

**► If the target has already developed one breast cancer, the breast cancer risks describe the likelihood of developing a contralateral breast cancer.**

**► The risks computed by BOADICEA are 'remaining lifetime' risks. A remaining lifetime risk is the risk of cancer occurring between the individual's current age and 80 (say for an individual in their 30s or 40s), conditional on the disease experience of the individual up to that point (whether she has remained unaffected or developed unilateral breast cancer).**

Additional information on interpreting results is available in the Frequently Asked Questions section of the BOADICEA Web site.

# 7. SAVING RESULTS

When you have run your BOADICEA risk calculation, you can generate a set of output data files to save on your computer. To do this, press the 'Generate Report' button on the COMPUTED RESULTS Web page (Figure 13). In a few seconds, the program will return a PROCESSING REPORT Web page (Figure 14).

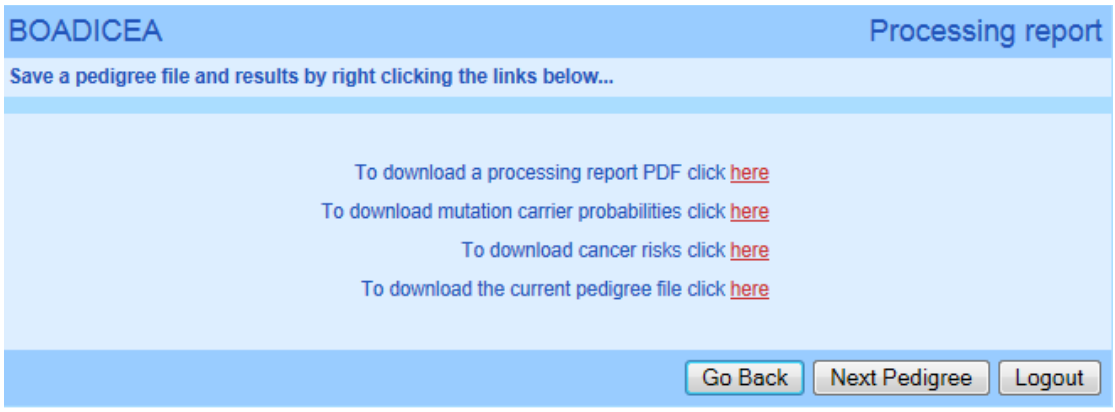

BOADICEA
Processing report
Save a pedigree file and results by right clicking the links below...
To download a processing report PDF click here
To download mutation carrier probabilities click here
To download cancer risks click here
To download the current pedigree file click here
Go Back
Next Pedigree
Logout

**Figure 14. The PROCESSING REPORT Web page.**

The PROCESSING REPORT Web page (Figure 14) includes links that enable you to download the following files to your local computer for archival purposes:

- Processing report PDF
- BRCA mutation carrier probabilities
- Breast/ovarian cancer risks
- Current pedigree data set

These options are described below.

## 7.1 Processing report PDF

The BWA program summarises your latest risk calculation in a processing report PDF (Figure 15). To download this document, right click here in the first line of text on the PROCESSING REPORT Web page (Figure 14), and select 'Save Target As…' in your browser menu. When you have specified an output data filename, the document will be downloaded to your computer via a secure Internet connection.

The processing report PDF includes the following:

- Processing report summary and pedigree data table
- Pedigree drawing
- Computed results and model parameters
- Breast/ovarian cancer risk graphs

The processing report summary is written at the start of the report (at the top of the page, Figure 15). It includes the date and time of the risk calculation, the session and risk calculation numbers, and details of the input pedigree and target.

**► The session number and risk calculation number uniquely identify each BOADICEA risk calculation.**

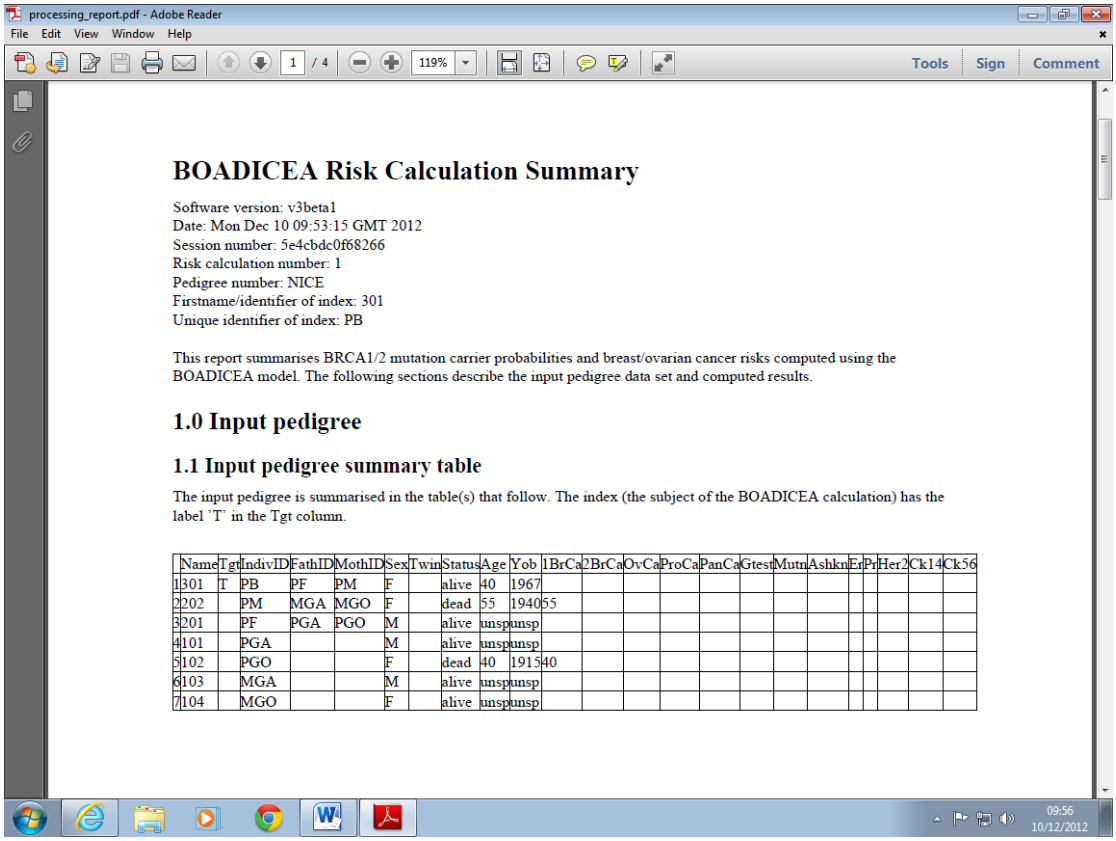

processing_report.pdf - Adobe Reader
File Edit View Window Help
Tools Sign Comment
BOADICEA Risk Calculation Summary
Software version: v3beta1
Date: Mon Dec 10 09:53:15 GMT 2012
Session number: 5e4cbdc0f68266
Risk calculation number: 1
Pedigree number: NICE
Firstname/identifier of index: 301
Unique identifier of index: PB
This report summarises BRCA1/2 mutation carrier probabilities and breast/ovarian cancer risks computed using the BOADICEA model. The following sections describe the input pedigree data set and computed results.
1.0 Input pedigree
1.1 Input pedigree summary table
The input pedigree is summarised in the table(s) that follow. The index (the subject of the BOADICEA calculation) has the label 'T' in the Tgt column.
Name Tgt IndivID FathID MothID Sex Twin Status Age Yob 1BrCa 2BrCa OvCa ProCa PanCa Gtest Mutn Ashkn Er Pr Her2 Ck14 Ck56
1 301 T PB PF PM F alive 40 1967
2 202 PM MGA MGO F dead 55 194055
3 201 PF PGA PGO M alive unspunsp
4 101 PGA M alive unspunsp
5 102 PGO F dead 40 191540
6 103 MGA M alive unspunsp
7 104 MGO F alive unspunsp
09:56
10/12/2012

**Figure 15. The processing report PDF.**

## 7.2 BRCA mutation carrier probabilities

The BWA program stores the computed BRCA1 and BRCA2 mutation carrier probabilities from the latest processing run in an export data file. The carrier probabilities are listed in the file in a simple TAB delimited plain text format (see Appendix C for more details). This data file also includes the session number and risk calculation number, which means that you will always be able to link the mutation carrier probabilities written in your processing report PDF and export data file.

To download the mutation carrier probabilities data file, right click here in the second line of text on the PROCESSING REPORT Web page (Figure 14), and select 'Save Target As…' in your browser menu. When you have specified an output data filename, the data will be downloaded to you computer via a secure Internet connection.

## 7.3 Breast and ovarian cancer risks

The BWA program stores your computed breast/ovarian cancer risks from the latest processing run in an export data file. The cancer risks are listed in the file in a simple TAB delimited plain text format (see Appendix D for more details). This data file also includes the session number and risk calculation number, which means that you will always be able to link breast and ovarian cancer risks written in your processing report PDF and export data file.

To download this data file, right click here in the third line of text on the PROCESSING REPORT Web page (Figure 14), and select 'Save Target As…' in your browser menu. When you have specified an output data filename, the data will be downloaded to you computer via a secure Internet connection.

## 7.4 Pedigree data

The BWA program stores your current pedigree set in BOADICEA I/E format. To download the pedigree file, right click here in the fourth line of text on the PROCESSING REPORT Web page (Figure 14), and select 'Save Target As…' in your browser menu. When you have specified an output data filename, the pedigree will be downloaded to you computer via a secure Internet connection.

If you have built a new pedigree data set online, these data will be saved in the download file. Alternatively, if you have uploaded a pre-existing pedigree data set for processing and amended it online, the amended data will be saved in the download file.

The downloaded pedigree data set will be stored on your computer in BOADICEA I/E format. Consequently, you can upload it, amend it online, and reprocess it again at any time in the future.

**► We strongly recommend that users save a copy of all results files for archival purposes.**

# 8. BATCH PROCESSING

The BWA includes a batch processing module that enables you to upload a BOADICEA I/E data file containing multiple pedigree data sets and to process them in a single processing run. If you upload a text file with two or more pedigree data sets, the program will detect that multiple pedigree data sets are present in the file and will generate a CONFIRM PEDIGREE DATA VALIDATION Web page (Figure 16).

**► Batch pedigree data files can contain up to 500 separate pedigrees**

**► Batch pedigree data files can have a maximum size of 60 MB**

**► The model parameter settings used when batch processing are not recorded in the output data files. As a result, we strongly recommend that you make a record of these parameters whenever you submit a batch processing job.**

When batch processing for the first time, we recommend that you begin by submitting a small test batch pedigree data file for processing first (e.g. containing say 50 pedigrees). By running an initial test in this way, you can examine the results of the pedigree data validation process (described below) to identify any potential problems with your data. Please contact us if you would like further advice on batch processing (our contact details are here).

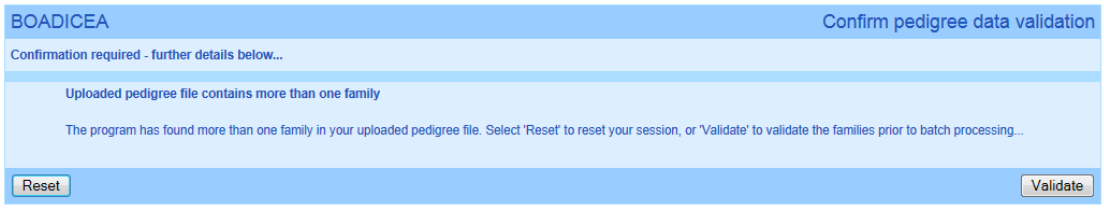

BOADICEA
Confirm pedigree data validation
Confirmation required - further details below...
Uploaded pedigree file contains more than one family
The program has found more than one family in your uploaded pedigree file. Select 'Reset' to reset your session, or 'Validate' to validate the families prior to batch processing...
Reset
Validate

**Figure 16. The CONFIRM PEDIGREE DATA VALIDATION Web page.**

Pedigree data sets submitted for batch processing are processed in two steps:

- Pedigree data validation
- Pedigree data processing

These activities are described below.

## 8.1 Pedigree validation

Before you compute BRCA mutation carrier probabilities and breast/ovarian cancer risks, you must first validate your input pedigree data sets. To do this, press the 'Validate' button on the CONFIRM PEDIGREE DATA VALIDATION Web page (Figure 16). This will initiate a batch processing job that will validate each pedigree data set in your BOADICEA I/E data file one after the other.

**► Each pedigree data set in your BOADICEA I/E file must be identified with a unique family identifier (FamID, described in Appendix A of this guide).**

When the batch job is running, the program will generate a BATCH PROCESSING JOB STATUS Web page (Figure 17) to keep you informed of progress.

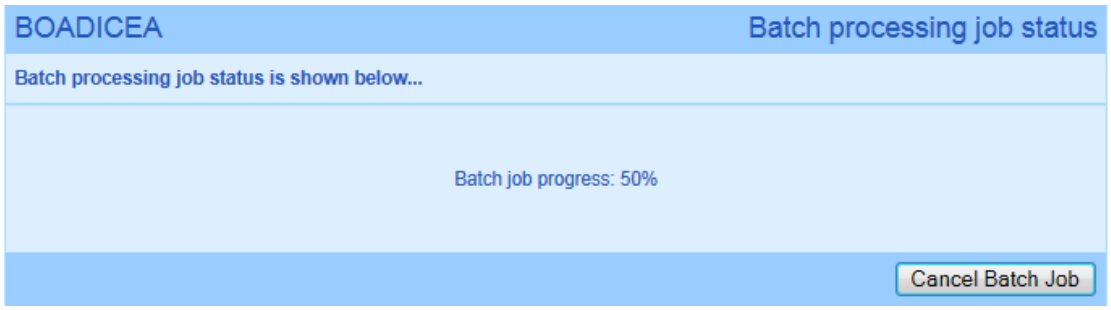



**Figure 17. The BATCH PROCESSING JOB STATUS Web page.**

When the pedigree validation batch job is complete, the BWA program will return a BATCH PROCESSING Web page (Figure 18).

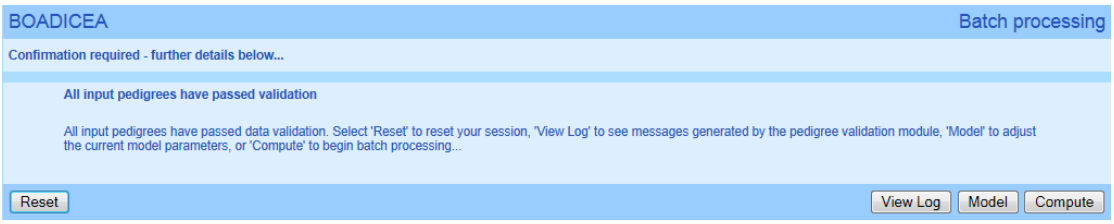

BOADICEA
Batch processing
Confirmation required - further details below...
All input pedigrees have passed validation
All input pedigrees have passed data validation. Select 'Reset' to reset your session, 'View Log' to see messages generated by the pedigree validation module, 'Model' to adjust the current model parameters, or 'Compute' to begin batch processing...
Reset
View Log
Model
Compute

**Figure 18. The BATCH PROCESSING Web page.**

The BATCH PROCESSING Web page enables you to do the following:

- Check the results of the pedigree validation batch job
- Adjust model parameters before a risk calculation
- Compute risks

These activities are described below.

### 8.1.1 Checking pedigree validation results

To check the results of the pedigree validation batch job, press the 'View Log' button. The program will then generate a VIEW PROCESSING LOG Web page (Figure 19).

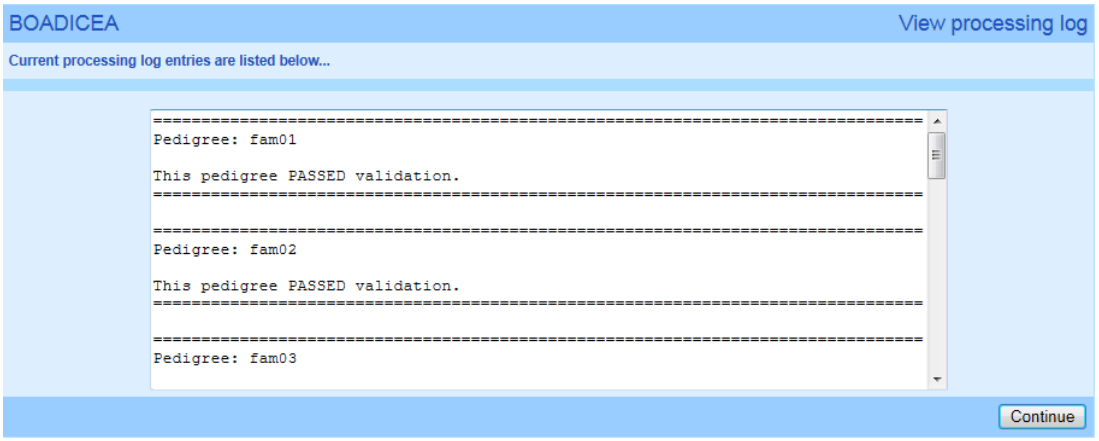



**Figure 19. The VIEW PROCESSING LOG Web page.**

The logfile identifies which pedigree data sets have passed validation.

## 8.2 Adjusting model parameters

If you wish, you can update the BOADICEA model parameters before you compute BRCA mutation carrier probabilities and breast/ovarian cancer risks. To do this, press the 'Model' button on the BATCH PROCESSING Web page (Figure 18). The program will then return a MODEL PARAMETERS Web page (Figure 12). See section 4 of this guide for further information on adjusting model parameters.

## 8.3 Computing risks

Once you have validated your input pedigree data sets, you can initiate a batch processing job to compute BRCA mutation carrier probabilities and breast/ovarian cancer risks by pressing the 'Compute' button on the BATCH PROCESSING Web page (Figure 18). The program will then generate a second BATCH PROCESSING JOB STATUS Web page (Figure 17) to keep you informed of progress.

## 8.4 Saving results

When the batch processing job has finished, the program will return a BATCH PROCESSING REPORT Web page (Figure 20).

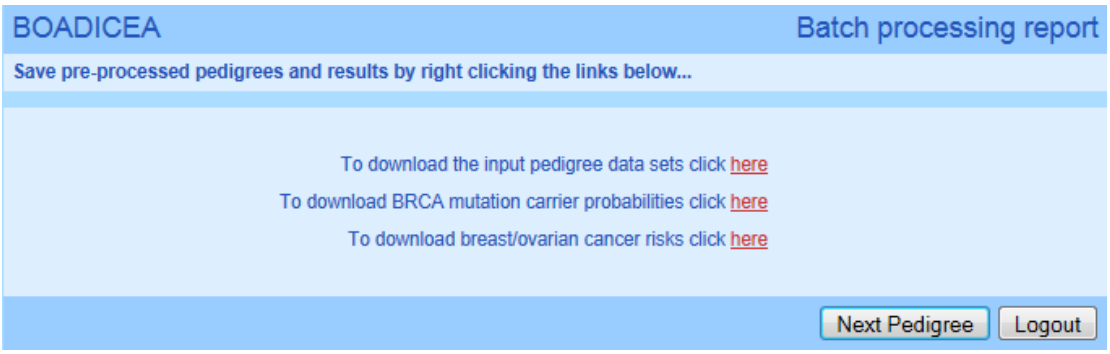

BOADICEA
Batch processing report
Save pre-processed pedigrees and results by right clicking the links below...
To download the input pedigree data sets click here
To download BRCA mutation carrier probabilities click here
To download breast/ovarian cancer risks click here
Next Pedigree
Logout

**Figure 20. The BATCH PROCESSING REPORT Web page.**

The BATCH PROCESSING REPORT Web page (Figure 20) includes links that enable you to download the following data files to your local computer for archival purposes:

- Input pedigree data sets in BOADICEA I/E format
- Computed BRCA mutation carrier probabilities
- Computed breast/ovarian cancer risks

These options are described below.

### 8.4.1 Pedigrees in BOADICEA import/export format

The BWA program provides a copy of the input pedigree data sets that passed validation and were submitted for processing in BOADICEA I/E format. To download this data file, right click here in the second line of text on the BATCH PROCESSING REPORT Web page (Figure 20), and select 'Save Target As…' in your browser menu.

### 8.4.2 BRCA mutation carrier probabilities

The BWA program stores the computed BRCA mutation carrier probabilities from the batch processing run in an export data file. The carrier probabilities are listed in the file in a simple TAB delimited plain text format (see Appendix C for more details). To download these data, right click here in the third line of text on the BATCH PROCESSING REPORT Web page (Figure 20), and select 'Save Target As…' in your browser menu.

### 8.4.3 Breast and ovarian cancer risks

The BWA program stores the computed breast/ovarian cancer risks from the batch processing run in an export data file. The breast/ovarian cancer risks are listed in the file in a simple TAB delimited plain text format (see Appendix D for more details). To download these data, right click here in the fourth line of text on the BATCH PROCESSING REPORT Web page (Figure 20), and select 'Save Target As…' in your browser menu.

# 9. LOGGING OUT

When you have saved your results, you can either reset the session by selecting the 'Next Pedigree' button on the PROCESSING REPORT (Figure 14) or BATCH PROCESSING REPORT Web page (Figure 20). Alternatively, you can terminate your session from either of these Web pages by pressing the 'Logout' button. If you select the 'Next Pedigree' button, the program will return you to the SESSION OPTION Web page (Figure 2). Alternatively, if you select the 'Logout' button, the program will return a SESSION COMPLETED Web page (Figure 21).

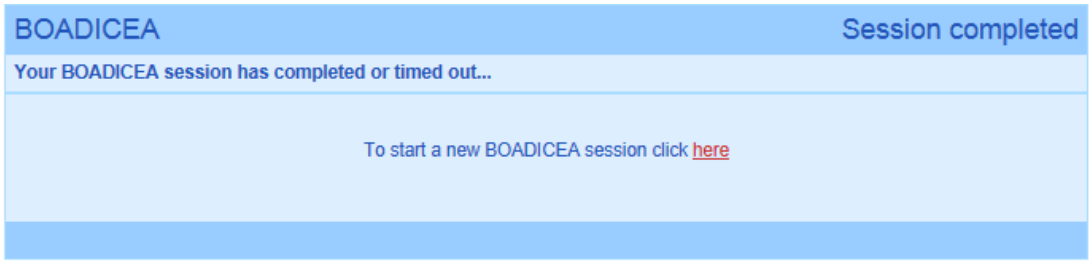

BOADICEA
Session completed
Your BOADICEA session has completed or timed out...
To start a new BOADICEA session click here

**Figure 21. The SESSION COMPLETED Web page.**

When you reset your session or logout, all data files created up to that point on the Web server are deleted. If you fail to logout and you loose your Internet connection, all data files on the Web server will be deleted 24 hours later. This helps us to conform to UK data protection principles.

# References

Zhao, J.H. 2006. Pedigree-drawing with R and graphviz, *Bioinformatics*, **22** (8), 1013-1014.

# Appendix A
# BOADICEA import/export pedigree data format (continued next page)

The BOADICEA import/export data format is described below. Each pedigree data record includes 24 data parameters separated by TAB or whitespace characters. Parameters 1-19 are shown below:

BOADICEA import pedigree file format 2.0

| FamID | Name | Target | IndivID | FathID | MothID | Sex | Twin | Dead | Age | Yob | 1BrCa | 2BrCa | OvCa | ProCa | PanCa | Gtest | Mutn | Ashkn… |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| uf9 | Clive | 0 | 101 | 0 | 0 | M | 0 | 0 | 92 | 1914 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| uf9 | Rose | 0 | 102 | 0 | 0 | F | 0 | 1 | 40 | 1915 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| uf9 | Alison | 0 | 301 | 201 | 202 | F | 0 | 0 | 32 | 1974 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| uf9 | Peter | 0 | 103 | 0 | 0 | M | 0 | 1 | 60 | 1915 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| uf9 | Jenny | 0 | 104 | 0 | 0 | F | 0 | 1 | 59 | 1913 | 0 | 0 | 58 | 0 | 0 | 0 | 0 | 0 |
| uf9 | Alan | 0 | 201 | 101 | 102 | M | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| uf9 | Sarah | 0 | 202 | 103 | 104 | F | 3 | 1 | 55 | 1944 | 53 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| uf9 | Amy | 0 | 203 | 103 | 104 | F | 3 | 0 | 62 | 1944 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| uf9 | Clare | 1 | 204 | 103 | 104 | F | 0 | 0 | 60 | 1946 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| uf9 | Mary | 0 | 302 | 201 | 202 | F | 0 | 0 | 30 | 1976 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Data fields should be separated by tab or whitespace characters only. Items highlighted in blue are required for the BOADICEA risk calculation. Other items are used for pedigree drawing, or to ensure forward compatibility with future versions of the software. Please note:

(1) The first line of text 'BOADICEA import pedigree file format 2.0' must be included, and the file version number must be set to 2 or 2.0.
(2) A second line of text must be included before the pedigree data records begin. We recommend that this shows column names as above.
(3) In BOADICEA import/export data files, each family member must have either no parents specified, or both parents specified.
(4) The IDs used to define family structure (IndivID, FathID and MothID) are case sensitive.

| | |
|---|---|
| FamID | Family/pedigree ID, character string (maximum 13 characters) |
| Name: | First name/ID of the family member, character string (maximum 8 characters) |
| Target: | The family member for whom the BOADICEA risk calculation is made, 1 = target for BOADICEA risk calculation, 0 = other family members. There must only be one BOADICEA target individual. |
| IndivID: | Unique ID of the family member, character string (maximum 7 characters) |
| FathID: | Unique ID of their father, 0 = no father, or character string (maximum 7 characters) |
| MothID: | Unique ID of their mother, 0 = unspecified, or character string (maximum 7 characters) |
| Sex: | M or F |
| Twin: | Identical twins, 0 = no identical twin, Use any one of these characters to identify MZ twins: 1 2 3 4 5 6 7 8 9 A. In the example pedigree above, Sarah and Amy are listed as identical twins. |
| Dead: | The current status of the family member, 0 = alive, 1 = dead |
| Age: | Age at last follow up, 0 = unspecified, integer = age at last follow up |
| Yob: | Year of birth, 0 = unspecified, or integer (consistent with Age if the person is alive) |
| 1BrCa | Age at first breast cancer diagnosis, 0 = unaffected, integer = age at diagnosis, AU = unknown age at diagnosis (affected unknown) |
| 2BrCa | Age at contralateral breast cancer diagnosis, 0 = unaffected, integer = age at diagnosis, AU = unknown age at diagnosis (affected unknown) |
| OvCa | Age at ovarian cancer diagnosis, 0 = unaffected, integer = age at diagnosis, AU = unknown age at diagnosis (affected unknown) |
| ProCa | Age at prostate cancer diagnosis 0 = unaffected, integer = age at diagnosis, AU = unknown age at diagnosis (affected unknown) |
| PanCa | Age at pancreatic cancer diagnosis 0 = unaffected, integer = age at diagnosis, AU = unknown age at diagnosis (affected unknown) |
| Gtest | Genetic test status, 0 = untested, S = mutation search, T = direct gene test |
| Mutn | 0 = untested, N = no mutation, 1 = BRCA1 positive, 2 = BRCA2 positive, 3 = BRCA1 and BRCA2 positive |
| Ashkn | 0 = not Ashkenazi, 1 = Ashkenazi |

# Appendix A
# BOADICEA import/export pedigree data format (continued from previous page)

Parameters 20-24 are shown below:

```
…       ER      PR      HER2    CK14    CK56
        0       0       0       0       0

ER      Estrogen receptor status, 0 = unspecified, N = negative, P = positive
PR      Progestrogen receptor status, 0 = unspecified, N = negative, P = positive
HER2    Human epidermal growth factor receptor 2 status, 0 = unspecified, N = negative, P = positive
CK14    Cytokeratin 14 status, 0 = unspecified, N = negative, P = positive
CK56    Cytokeratin 56 status, 0 = unspecified, N = negative, P = positive
```

# Appendix B
# Modifying BOADICEA import/export pedigree files

The BWA enables you to download pedigree data files that you have built online in BOADICEA I/E pedigree format. In many cases, you may wish to modify these files offline and reload them in order to run an updated risk calculation. You can edit BOADICEA I/E pedigree files as follows:

1. Read the BOADICEA import/export data file into *Microsoft Excel* by selecting:

File→Open, with Files of Type→Text Files

2. In the Text Import Wizard:

Step 1 of 3 Click 'Next'
Step 2 of 3 Select the Tab and Space checkboxes, and click 'Next'
Step 3 of 3 Select 'Finish'

3. Edit your data as required

4. Save the data by selecting:

File→Save As, with Save as Type→Text (tab delimited)

*Microsoft Excel* generates a warning at this point, click 'Yes' to save your spreadsheet to a new BOADICEA I/E pedigree file. You can then upload this new file to the Web server to run an updated risk calculation.

# Appendix C
# BOADICEA BRCA mutation carrier probabilities export data file format

The BOADICEA BRCA mutation carrier probabilities export data file format is as follows:

| FamID | Date | Time | SessionNum | CalNum | Name | IndivID | Version | BRCA1 | BRCA1% | BRCA2 | BRCA2% | NoMutation | NoMutation% |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 54273 | 10/12/12 | 14:42:15 | 069bc38144b562 | 1 | Alison | 1 | v3beta | 0.0200 | 2.0 | 0.0316 | 3.2 | 0.9484 | 94.8 |

| | |
|---|---|
| FamID: | Family/pedigree ID |
| Date: | Day of risk calculation |
| Time: | Time of risk calculation |
| SessionNum: | Session number, unique number generated when the user logs onto the server |
| CalcNum: | Risk calculation number, increments each time the user runs a risk calculation |
| Name: | Firstname/ID of the target (index or subject of the risk calculation) |
| IndivID: | Unique identifier of the target |
| BRCA1: | BRCA1 mutation carrier probability in decimal format |
| BRCA1%: | BRCA1 mutation carrier probability in percent format |
| BRCA2: | BRCA2 mutation carrier probability in decimal format |
| BRCA2%: | BRCA2 mutation carrier probability in percent format |
| NoMutation: | Probability of no mutation on decimal format |
| NoMutation%: | Probability of no mutation on percent format |

# Appendix D
# BOADICEA breast/ovarian cancer risks export data file format

The BOADICEA breast/ovarian cancer risks export data file format is as follows:

| FamID | Date | Time | SessionNum | CalNum | Name | IndivID | Version | Age | BrCaRisk | BrCaRisk% | OvCaRisk | OvCaRisk% |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 54273 | 10/12/12 | 14:42:15 | 069bc38144b562 | 1 | Alison | 1 | v3beta1 | 45 | 0.0043 | 0.4 | 0.0003 | 0.0 |
| 54273 | 10/12/12 | 14:42:15 | 069bc38144b562 | 1 | Alison | 1 | v3beta1 | 46 | 0.0089 | 0.9 | 0.0006 | 0.1 |
| 54273 | 10/12/12 | 14:42:15 | 069bc38144b562 | 1 | Alison | 1 | v3beta1 | 47 | 0.0138 | 1.4 | 0.0010 | 0.1 |
| 54273 | 10/12/12 | 14:42:15 | 069bc38144b562 | 1 | Alison | 1 | v3beta1 | 48 | 0.0191 | 1.9 | 0.0014 | 0.1 |
| 54273 | 10/12/12 | 14:42:15 | 069bc38144b562 | 1 | Alison | 1 | v3beta1 | 49 | 0.0246 | 2.5 | 0.0018 | 0.2 |
| 54273 | 10/12/12 | 14:42:15 | 069bc38144b562 | 1 | Alison | 1 | v3beta1 | 50 | 0.0303 | 3.0 | 0.0022 | 0.2 |
| 54273 | 10/12/12 | 14:42:15 | 069bc38144b562 | 1 | Alison | 1 | v3beta1 | 54 | 0.0541 | 5.4 | 0.0043 | 0.4 |
| 54273 | 10/12/12 | 14:42:15 | 069bc38144b562 | 1 | Alison | 1 | v3beta1 | 55 | 0.0600 | 6.0 | 0.0051 | 0.5 |
| 54273 | 10/12/12 | 14:42:15 | 069bc38144b562 | 1 | Alison | 1 | v3beta1 | 60 | 0.0902 | 9.0 | 0.0090 | 0.9 |
| 54273 | 10/12/12 | 14:42:15 | 069bc38144b562 | 1 | Alison | 1 | v3beta1 | 65 | 0.1222 | 12.2 | 0.0130 | 1.3 |
| 54273 | 10/12/12 | 14:42:15 | 069bc38144b562 | 1 | Alison | 1 | v3beta1 | 70 | 0.1530 | 15.3 | 0.0170 | 1.7 |
| 54273 | 10/12/12 | 14:42:15 | 069bc38144b562 | 1 | Alison | 1 | v3beta1 | 75 | 0.1788 | 17.9 | 0.0212 | 2.1 |
| 54273 | 10/12/12 | 14:42:15 | 069bc38144b562 | 1 | Alison | 1 | v3beta1 | 80 | 0.2014 | 20.1 | 0.0255 | 2.5 |

FamID: Family/pedigree ID, character string
Date: Day of risk calculation
Time: Time of risk calculation
SessionNum: Session number, unique number generated when the user logs into the server
CalcNum: Risk calculation number, increments each time the user runs a risk calculation
Name: Firstname/ID of the target (index or subject of the risk calculation)
IndivID: Unique identifier of the target
Version: BOADICEA Web Application version number
Age: Age at last follow up of target (current age or age at death, maximum 3 characters)
BrCaRisk: Breast cancer risk in decimal format
BrCaRisk%: Breast cancer risk in percent format
OvCaRisk: Ovarian cancer risk in decimal format
OvCaRisk%: Ovarian cancer risk in percent format